

## **FIGURE 106**

A.

### **SEQ ID NO:67 - AME 33 complete light chain amino acid sequence**

EIVLTQSPGTLSLSPGERATLSCRASSVPYIHWYQQKPGQAPRLLIYATSALASGIPDR  
FSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIKRTVAAAPSVFIFPPS  
DEQLKSGTASVVCLNNFPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST  
LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

- Constant Region is underlined

B.

### **SEQ ID NO:68 - AME 33 complete light chain nucleic acid sequence**

GAAATTGTGTTACGCAGTCCTCCAGGCACCCGTCTTGCTCCAGGGAAAGAG  
CCACCCCTCTCCTGCAGGCCAGCTCAAGTGTACCGTACATCCACTGGTACCAGCA  
GAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCTGGCTCTG  
GCATCCCAGACAGGTTCAGTGGCAGTGGCTCTGGGACAGACTTCACTCTCACCAT  
CAGCAGACTGGAGCCTGAAGATTTGCAGTGTATTACTGTCACTGGCTGAGT  
AACCCACCCACTTGGCCAGGGACCAAGCTGGAGATCAAACGAACGTGGCTG  
CACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACGTGCC  
TCTGTTGTGTCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG  
AGGTGGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACAGAGCAGGA  
CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCGTGACGCTGAGCAAAGCAGA  
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCTGAGCTCG  
CCCGTCACAAAGAGCTAACAGGGAGAGTGTAG

## FIGURE 117

### A. SEQ ID NO:69 - AME 33 complete heavy chain amino acid sequence

EVQLVQSGAEVKPGESLKISCKSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTG  
DTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWG  
KGTTTVSSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVWSNSGALTSG  
VHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTH  
TCPPCPAPELLGGPSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV  
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA  
KGQPREPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPV  
LSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

- Constant Region is underlined; the "D" at position 280 and "K" at position 290 are in bold

### B. SEQ ID NO:70 - AME 33 complete heavy chain nucleic acid sequence

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCAGGGAGTCTCTG  
AAGATCTCCTGTAAGGGTCTGGCCGTACATTACCAAGTTACAATATGCACTGGGT  
GCGCCAGATGCCGGAAAGGCCTGGAGTGGATGGGGCTATTATCCCTGACG  
GGTGATACTTCCTACAATCAGAACGACTCCAGGTACCCTCAGCCGACA  
AGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTGGACACCGC  
CATGTATTACTGTGCGAGATCGACTACGTGGCGGTGACTGGCAGTCAGTGTCT  
GGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCATCGGT  
CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCT  
GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTACTGGCAGTCAG  
CCTGACCAGCGCGTGCACACCTCCGGCTGTCTACAGTCCTCAGGACTCTACT  
CCCTCAGCAGCGTGGTGACCGTGCCCCAGCAGCTGGGACCCAGACCTACAT  
CTGCAACGTGAATACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTTGAGCC  
CAAATCTTGTGACAAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTG  
GGGGGACCGTCAGTCTCCTCTCCCCCAAAACCCAGGACACCCTCATGATCTC  
CCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAG  
GTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAG  
CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCGTCC  
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCCAAACAAAG  
CCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGA  
ACCACAGGTGTACACCCTGCCCAATCCCAGGACGAGCTGACCAAGAACCAAGGTC  
AGCCTGACCTGCCTGGTCAAAGGCTCTATCCAGCGACATGCCGTGGAGTGGG  
AGAGCAATGGGCAGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCGTGTGGACTC  
CGACGGCTCCTCTTCTCATGCAAGCTACCGTGGACAAGAGCAGGTGGCAG  
CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA  
CGCAGAAGAGCCTCTCCGTCTCCGGTAAATGA